

DAYER
SEQUENCE LISTING

<110> Dayer, Jean-Michel
Burger, Danielle
Kohno, Tadahiko
Edwards III, Carl K.

<120> APO-A-1 REGULATION OF T-CELL SIGNALING

<130> 06843.0035-00000

<140> Not Yet Assigned

<141> 2001-03-13

<150> 60/189,008

<151> 2000-03-13

<150> 60/193,551

<151> 2000-03-31

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 801

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> (20)..(91)

<400> 1

```

atgaaagctg cggtgctgac cttggccgtg ctcttctcta cggggagcca ggctcggcat 79
ttctggcagc aagatgaacc cccccagagc ccctgggatc gagtgaagga cctggccact 139
gtgtacgtgg atgtgctcaa agacagcggc agagactatg tgtcccagtt tgaaggctcc 199
gccttgggaa aacagctaaa cctaaagctc cttgacaact gggacagcgt gacctccacc 259
ttcagcaagc tgcgcgaaca gctcggccct gtgacccagg agttctggga taacctggaa 319
aaggagacag agggcctgag gcaggagatg agcaaggatc tggaggagggt gaaggccaag 379
gtgcagccct acctggacga cttccagaag aagtggcagg aggagatgga gctctaccgc 439
cagaagggtg agccgctgcg cgcagagctc caagagggcg cgcgccagaa gctgcacgag 499
ctgcaagaga agctgagccc actgggcgag gagatgcgcg accgcgcgcg cgcccatgtg 559
gacgcgctgc gcacgcctct ggccccctac agcgacgagc tgcgccagcg cttggccgcg 619
cgccttgagg ctctcaagga gaacggcggc gccagactgg ccgagtacca cgccaaggcc 679
accgagcatc tgagcacgct cagcgagaag gccaaagccc cgctcgagga cctccgcca 739
ggcctgctgc ccgtgctgga gagcttcaag gtcagcttcc tgagcgctct cgaggagtac 799
actaagaagc tcaacacca g                                     820

```

<210> 2

<211> 267

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Lys Ala Ala Val Leu Thr Leu Ala Val Leu Phe Leu Thr Gly Ser
  1           5           10          15
Gln Ala Arg His Phe Trp Gln Gln Asp Glu Pro Pro Gln Ser Pro Trp
          20          25          30

```

DAYER

Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu Lys Asp
35 40 45

Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly Lys
50 55 60

Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser Thr
65 70 75 80

Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp
85 90 95

Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys
100 105 110

Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe
115 120 125

Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu
130 135 140

Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu
145 150 155 160

Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala
165 170 175

Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp
180 185 190

Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn
195 200 205

Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu
210 215 220

Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln
225 230 235 240

Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala
245 250 255

Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln
260 265

<210> 3
<211> 170
<212> PRT
<213> Homo sapiens
<220>
<221> PEPTIDE
<222> (1)..(170)
<223> 18 kDa N-terminal fragment

<400> 3
Asp Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr
1 5 10 15
Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln
20 25 30

DAYER

Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp
35 40 45

Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu
50 55 60

Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu
65 70 75 80

Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys
85 90 95

Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met
100 105 110

Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu
115 120 125

Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu
130 135 140

Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg
145 150 155 160

Thr His Leu Ala Pro Tyr Ser Asp Glu Leu
165 170

<210> 4
<211> 510
<212> DNA
<213> Homo sapiens

<400> 4
gatgaacccc cccagagccc ctgggatcga gtgaaggacc tggccactgt gtacgtggat 151
gtgctcaaag acagcggcag agactatgtg tcccagtttg aaggctccgc ctggggaaaa 211
cagctaaacc taaagctcct tgacaactgg gacagcgtga cctccacctt cagcaagctg 271
cgcgaacagc tcggccctgt gaccaggag ttctgggata acctggaaaa ggagacagag 331
ggcctgaggc aggagatgag caaggatctg gaggaggtga aggccaaggt gcagccctac 391
ctggacgact tccagaagaa gtggcaggag gagatggagc tctaccgcca gaaggtggag 451
ccgctgcgcg cagagctcca agagggcgcg cgccagaagc tgcacgagct gcaagagaag 511
ctgagcccac tgggcgagga gatgcgcgac cgcgcgcgcg cccatgtgga cgcgctgcgc 571
acgcatttgg cccctacag cgacgagctg 601